

In the Claims:

Please amend claim 21 and add new claims 30-33. Please cancel claims 1-20, 26, and 28-29. The claims and their status are shown below.

1-20. (Canceled)

21. (Currently Amended) A method for determining the presence or absence of an open reading frame in a nucleic acid molecule among a population of nucleic acid molecules, said method comprising:

a) inserting said nucleic acid molecule into a vector, said vector comprising an nucleic acid sequence, wherein said nucleic acid sequence comprises three start codons within a span of 50 nucleotides, wherein each said start codon is within a different reading frame, wherein said nucleic acid sequence encodes histidine tags in three reading frames, wherein said nucleic acid molecule is inserted into said vector the vector of claim 10 such that said nucleic acid molecule is 3' or 5' of said nucleic acid sequence encoding said histidine tags;

b) introducing the resulting vector into a host cell;

c) culturing said host cell under conditions permitting expression of said nucleic acid molecule;

d) determining the presence or absence of a histidine tagged polypeptide encoded by said nucleic acid molecule, the presence of a histidine tagged polypeptide indicating that said nucleic acid molecule has an open reading frame.

22. (Original) The method of claim 21, wherein said nucleic acid molecule is a genomic DNA fragment, an EST or a cDNA molecule.

23. (Original) The method of claim 21, wherein said host cell is a prokaryotic or an eukaryotic cell.

24. (Original) The method of claim 21, wherein said host cell is a plant or an animal cell.

25. (Original) The method of claim 21, wherein said host cell is a yeast or a bacterial cell.

26. (Canceled)

27. (Original) A method for isolating a polypeptide encoded by a nucleic acid molecule, comprising:

e) determining if said nucleic acid molecule encodes an open reading frame, using the method of claim 21;

f) isolating said histidine tagged polypeptide.

28-29. (Cancelled)

30. (New) The method of claim 21, wherein said start codons are ATG codons.

31. (New) The method of claim 21, wherein said start codons are within a span of 13 nucleotides.

32. (New) The method of claim 31, wherein said 13 nucleotides are ATGGCATGGCATG (SEQ ID NO. 19).

33. (New) The method of claim 21, wherein said isolated nucleic acid further comprises a ribosome-binding site positioned 5' of said start codons.